

OIPE

1/2

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/630,931

DATE: 08/16/2000  
 TIME: 12:58:59

Input Set : A:\elitra6A.txt  
 Output Set: N:\CRF3\08162000\I630931.raw

Does Not Comply  
 Corrected Diskette Needed

4 <110> APPLICANT: Zyskind, Judith W.  
 6 <120> TITLE OF INVENTION: CHITOBIASE AS A REPORTER ENZYME  
 8 <130> FILE REFERENCE: ELITRA.006A  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/630,931  
 C--> 10 <141> CURRENT FILING DATE: 2000-08-02  
 10 <150> PRIOR APPLICATION NUMBER: 60/159,221  
 12 <151> PRIOR FILING DATE: 1999-10-13  
 14 <160> NUMBER OF SEQ ID NOS: 19  
 16 <170> SOFTWARE: FastSEQ for Windows Version 4.0

## ERRORED SEQUENCES

861 <210> SEQ ID NO: 19  
 862 <211> LENGTH: 880  
 863 <212> TYPE: PRT  
 864 <213> ORGANISM: Artificial Sequence  
 866 <220> FEATURE:  
 867 <223> OTHER INFORMATION: dnaA/Chitobiase Fusion  
 869 <400> SEQUENCE: 19  
 870 Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu  
 871 1 5 10 15  
 872 Leu Val Pro Ser Ser Glu Gln Gln Val Val Asn Ser Leu Ala Asp Asn  
 873 20 25 30  
 874 Leu Asp Ile Gln Tyr Glu Val Leu Thr Asn His Gly Ala Asn Glu Gly  
 875 35 40 45  
 876 Leu Ala Cys Gln Asp Met Gly Ala Glu Trp Ala Ser Cys Asn Lys Val  
 877 50 55 60  
 878 Asn Met Thr Leu Val Asn Gln Gly Glu Ala Val Asp Ser Lys Asp Trp  
 879 65 70 75 80  
 880 Ala Ile Tyr Phe His Ser Ile Arg Leu Ile Leu Asp Val Asp Asn Glu  
 881 85 90 95  
 882 Gln Phe Lys Ile Ser Arg Val Thr Gly Asp Leu His Lys Leu Glu Pro  
 883 100 105 110  
 884 Thr Asp Lys Phe Asp Gly Phe Ala Ala Gly Glu Val Val Leu Pro  
 885 115 120 125  
 886 Leu Val Gly Glu Tyr Trp Gln Leu Phe Glu Thr Asp Phe Met Pro Gly  
 887 130 135 140  
 888 Ala Phe Val Ser Ala Pro Asn Ala Glu Pro Lys Met Ile Ala Ser Leu  
 889 145 150 155 160  
 890 Asn Thr Glu Asp Val Ala Ser Phe Val Thr Gly Leu Glu Gly Asn Asn  
 891 165 170 175  
 892 Leu Lys Arg Thr Pro Asp Asp Asn Val Phe Ala Asn Ala Val Ser  
 893 180 185 190  
 894 Arg Phe Glu Lys Asn Glu Asp Leu Ala Thr Gln Asp Val Ser Thr Thr  
 895 195 200 205  
 896 Leu Leu Pro Thr Pro Met His Val Glu Ala Gly Lys Gly Lys Val Asp

sls  
 P3

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|     |   |     |   |
|-----|---|-----|---|
| 897 | 210   | 215 | 220                                     |
| 898 | Ile Ala Asp Gly Ile Ala Leu Pro Lys Asp Ala Phe Asp Ala Thr Gln         | 230 | 235                                     |
| 899 | 225   | 240 | Arg Ala Glu Val Val Gly Val Asp Val Arg |
| 900 | Phe Ala Ala Ile Gln Asp Arg Ala   | 245 | 255                                     |
| 901 | Gly Asp Leu Pro Val Ser Ile Thr Val Val Pro Ala Asp Phe Thr Gly         | 250 |   |
| 902 | 260   | 265 |   |
| 903 | Glu Leu Ala Lys Ser Gly Ala Tyr Glu Met Ser Ile Lys Gly Asp Gly         | 275 | 280                                     |
| 904 | 285   |     |   |
| 905 | Ile Val Ile Lys Ala Phe Asp Gln Ala Gly Ala Phe Tyr Ala Val Gln         | 290 | 300                                     |
| 906 | 295   | 300 |   |
| 907 | Ser Ile Phe Gly Leu Val Asp Ser Gln Asn Ala Asp Ser Leu Pro Gln         | 310 | 320                                     |
| 908 | 315   |     |   |
| 909 | 305   | 325 | Tyr Arg Gly Val Met Val                 |
| 910 | Leu Ser Ile Lys Asp Ala Pro Arg Phe Asp Tyr Arg Gly Val                 | 330 | 335                                     |
| 911 | Ile Leu Ala Thr   | 345 | 350                                     |
| 912 | Asp Val Ala Arg Asn Phe His Ser Lys Asp Ala Ile Leu Ala Thr Leu         | 340 |   |
| 913 | 355   | 360 |   |
| 914 | Asp Gln Met Ala Ala Tyr Lys Met Asn Lys Leu His Leu His Leu Thr         | 365 |   |
| 915 | 370   | 375 |   |
| 916 | Asp Asp Glu Gly Trp Arg Leu Glu Ile Pro Gly Leu Pro Glu Leu Thr         | 380 |   |
| 917 | 385   |     |   |
| 918 | Glu Val Gly Ala Asn Arg Cys Phe Asp Thr Gln Glu Lys Ser Cys Leu         | 390 | 395                                     |
| 919 | 400   |     |   |
| 920 | Leu Pro Gln Leu Gly Ser Gly Pro Thr Thr Asp Asn Phe Gly Ser Gly         | 405 | 410                                     |
| 921 | 415   |     |   |
| 922 | Tyr Phe Ser Lys Ala Asp Tyr Val Glu Ile Leu Lys Tyr Ala Lys Ala         | 420 | 425                                     |
| 923 | 430   |     |   |
| 924 | Arg Asn Ile Glu Val Ile Pro Glu Ile Asp Met Pro Ala His Ala Arg         | 435 | 440                                     |
| 925 | 445   |     |   |
| 926 | Ala Ala Val Val Ser Met Glu Ala Arg Tyr Asp Arg Leu Met Glu Glu         | 450 | 455                                     |
| 927 | 460   |     |   |
| 928 | Gly Lys Glu Ala Glu Ala Asn Glu Tyr Arg Leu Met Asp Pro Gln Asp         | 470 | 475                                     |
| 929 | 480   |     |   |
| 930 | Leu Pro Ser Asn Val Thr Thr Val Gln Phe Tyr Asn Lys Gln Ser Phe Ile     | 485 | 490                                     |
| 931 | 495   |     |   |
| 932 | Thr Ser Asn Pro Cys Met Glu Ser Ser Thr Arg Phe Val Asp Lys Val Ile Ser | 500 | 505                                     |
| 933 | 510   |     |   |
| 934 | Glu Val Ala Ala Met His Gln Glu Ala Gly Ala Pro Leu Thr Trp             | 515 | 520                                     |
| 935 | 525   |     |   |
| 936 | His Phe Gly Gly Asp Glu Ala Lys Asn Ile Lys Leu Gly Ala Gly Phe         | 530 | 535                                     |
| 937 | 540   |     |   |
| 938 | Gln Asp Val Asn Ala Glu Asp Lys Val Ser Trp Lys Gly Thr Ile Asp         | 550 | 555                                     |
| 939 | 560   |     |   |
| 940 | Leu Ser Lys Gln Asp Lys Pro Phe Ala Gln Ser Pro Gln Cys Gln Thr         | 565 | 570                                     |
| 941 | 575   |     |   |
| 942 | Leu Ile Thr Asp Gly Thr Val Ser Asp Phe Ala His Leu Pro Ser His         | 580 | 585                                     |
| 943 | 590   |     |   |
| 944 | Phe Ala Glu Glu Val Ser Lys Ile Val Ala Glu Lys Gly Ile Pro Asn         | 595 | 600                                     |
| 945 | 605   |     |   |

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946 Phe Gln Ala Trp Gln Asp Gly Leu Lys Tyr Ser Asp Gly Glu Lys Ala  
 610 615 620  
 947 625 625 630 635 640  
 948 Phe Ala Thr Glu Asn Thr Arg Val Asn Phe Trp Asp Val Leu Tyr Trp  
 950 Gly Gly Thr Ser Ser Val Tyr Glu Trp Ser Lys Lys Gly Tyr Asp Val  
 951 645 650 655  
 952 Ile Val Ser Asn Pro Asp Tyr Val Tyr Met Asp Met Pro Tyr Glu Val  
 660 665 670  
 953 675 680 685  
 954 Asp Pro Lys Glu Arg Gly Tyr Tyr Trp Ala Thr Arg Ala Thr Asp Thr  
 955 690 695 700  
 956 Arg Lys Met Phe Gly Phe Ala Pro Glu Asn Met Pro Gln Asn Ala Glu  
 957 705 710 715 720  
 958 Thr Ser Val Asp Arg Asp Gly Asn Gly Phe Thr Gly Lys Gly Glu Ile  
 959 725 730 735  
 960 Glu Ala Lys Pro Phe Tyr Gly Leu Ser Ala Gln Leu Trp Ser Glu Thr  
 961 740 745 750  
 962 Val Arg Asn Asp Glu Gln Tyr Glu Tyr Met Val Phe Pro Arg Val Leu  
 963 755 760 765  
 964 Ala Ala Ala Gln Arg Ala Trp His Arg Ala Asp Trp Glu Asn Asp Tyr  
 965 770 775 780  
 966 Lys Val Gly Val Glu Tyr Ser Gln Asn Ser Asn Leu Val Asp Lys Ala  
 967 785 790 795 800  
 968 Ser Leu Asn Gln Asp Tyr Asn Arg Phe Ala Asn Val Leu Gly Gln Arg  
 969 805 810 815  
 970 Glu Leu Ala Lys Leu Glu Lys Ser Gly Ile Asp Tyr Arg Leu Pro Val  
 971 820 825 830  
 972 Pro Gly Ala Lys Val Glu Asp Gly Lys Leu Ala Met Asn Val Gln Phe  
 973 835 840 845  
 974 Pro Gly Val Thr Leu Gln Tyr Ser Leu Asp Gly Glu Asn Trp Leu Thr  
 975 850 855 860  
 976 Tyr Ala Asp Asn Ala Arg Pro Asn Val Thr Gly Glu Val Phe Ile Arg  
 977 865 870 875 880  
 978 Ser Val Ser Ala Thr Gly Glu Lys Val Ser Arg Ile Thr Ser Val Lys  
 979 880

E--> 981 18  
E--> 984 1

*delete at end of file*

*See next page for more errors*

09/630,931

4

<210> 15  
<211> 238  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> LacZ(/chitobiase Fusion

<220> 238 ← only 238 nucleotides in sequence 15  
<221> CDS  
<222> (119) ... (240)

<221> -35\_signal  
<222> (44) ... (50)  
<223> Lac promoter

<221> -10\_signal  
<222> (69) ... (74)  
<223> Lac promoter  
<221> protein\_bind  
<222> (81) ... (107)  
<223> Lac repressor binding site

<221> protein\_bind  
<222> (7) ... (34)  
<223> CAP-cAMP binding site

<400> 15  
gcatgcatta atgtgagttt gctcactcat taggcacccccc aggcttaca ctttatgctt 60  
ccggctcgta tggatgtgg aatttgagc ggataacaat ttcacacagg aaacagct 118  
atg acc atg att acg cca agc ttg cat gcc tgc agg tcg act cta gag 166  
Met Thr Met Ile Thr Pro Ser Leu His Ala Cys Arg Ser Thr Leu Glu  
1 5 10 15

gat ccc cgg gta ccg agc tct gag caa caa gtt gta aac tca ctg gct 214  
Asp Pro Arg Val Pro Ser Ser Glu Gln Gln Val Val Asn Ser Leu Ala  
20 25 30

gat aac ctt gat atc caa tat gaa  
Asp Asn Leu Asp Ile Gln Tyr Glu  
35 40

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VERIFICATION SUMMARY  
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Input Set : A:\elitra6A.txt  
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:61 M:283 W: Missing Blank Line separator, <210> field identifier  
L:346 M:283 W: Missing Blank Line separator, <210> field identifier  
L:560 M:283 W: Missing Blank Line separator, <220> field identifier, SEQ ID#:15, CDS LOCATION: (119)....(240)  
L:565 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID:19  
L:602 M:283 W: Missing Blank Line separator, <220> field identifier  
L:617 M:283 W: Missing Blank Line separator, <220> field identifier  
L:981 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:19  
M:332 Repeated in SeqNo=19